

FIG. 1

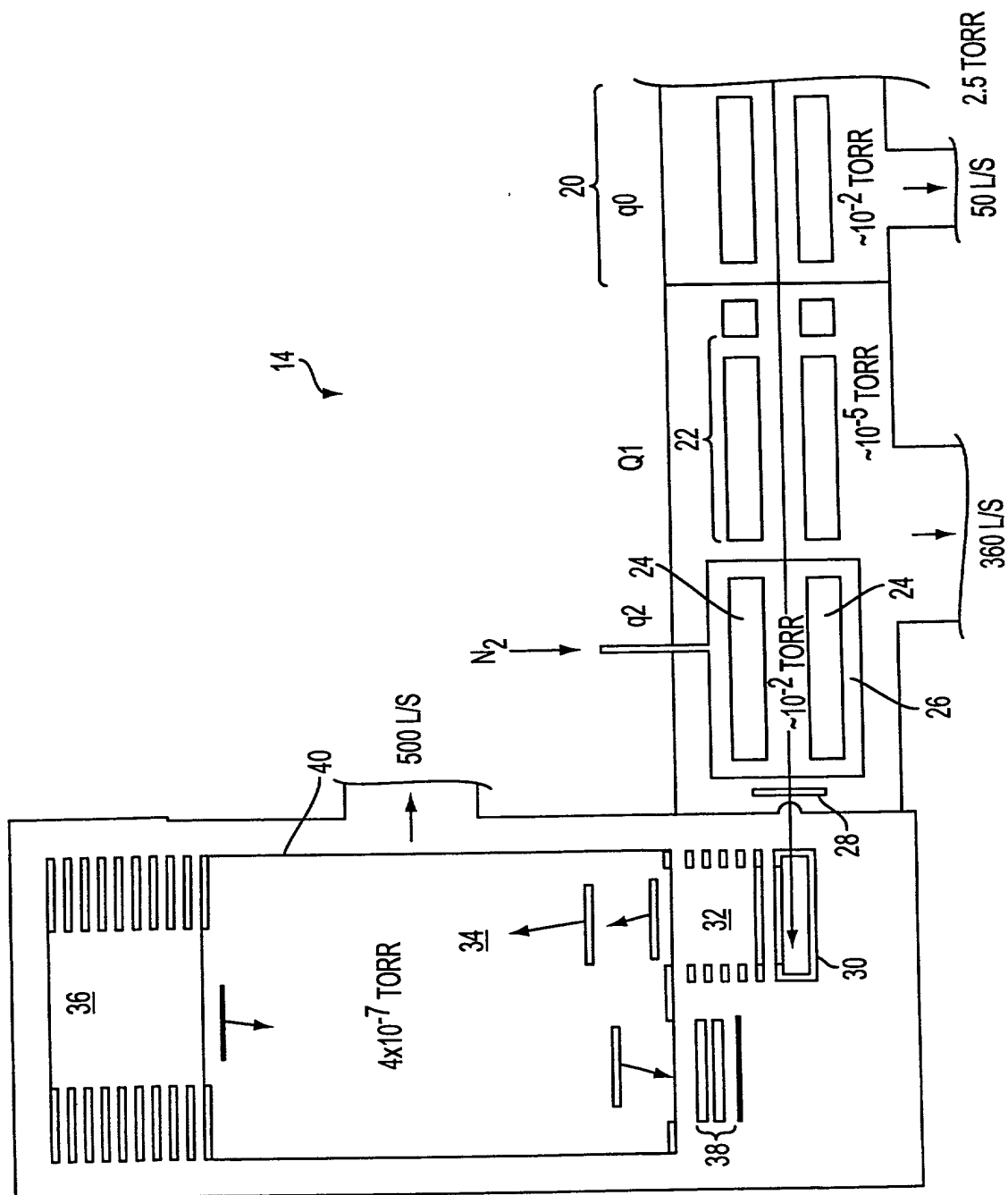


FIG. 2

Sheet 3 of 27

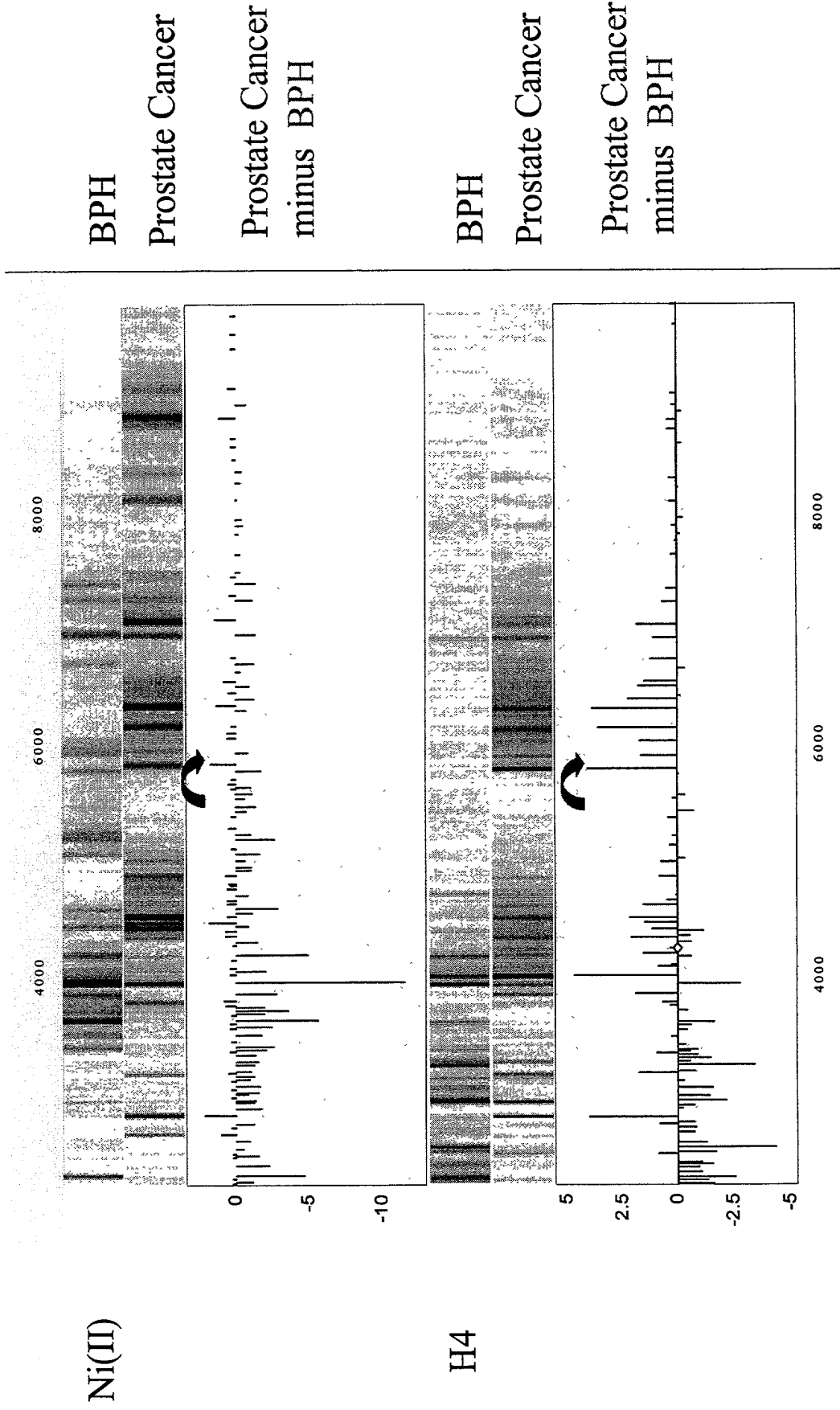


FIG. 3

Sheet 4 of 27

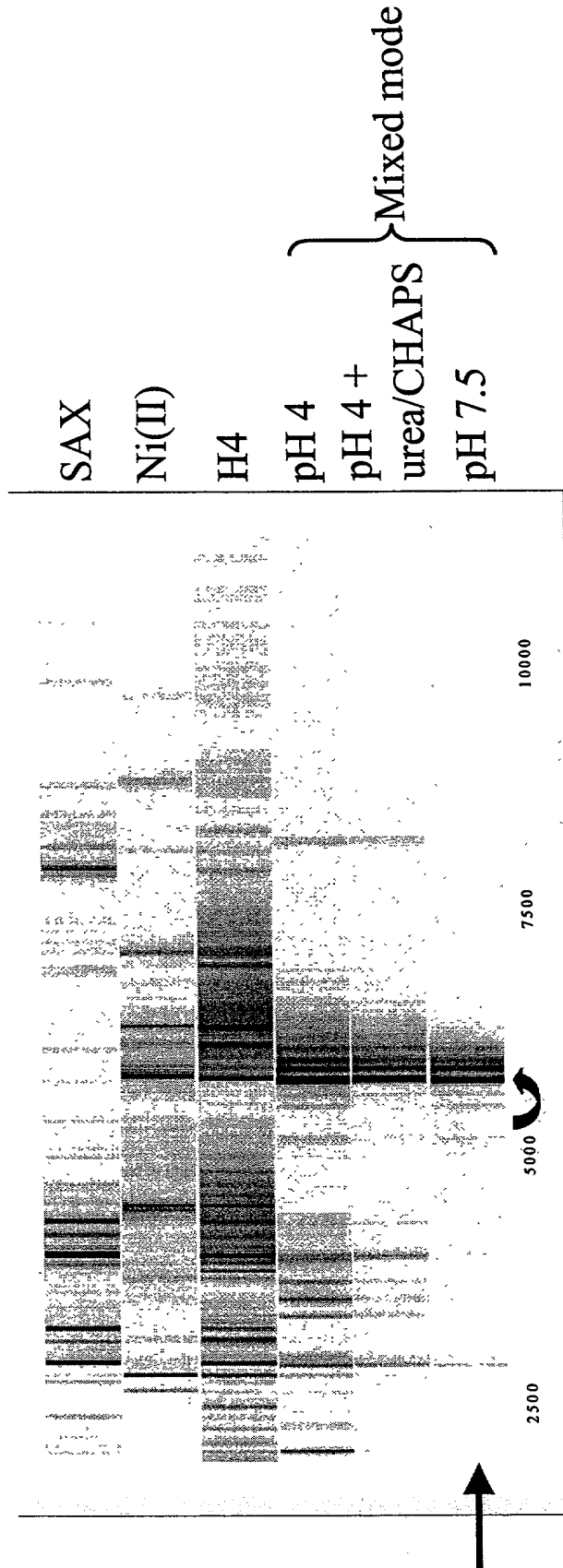


FIG. 4

Sheet 5 of 27

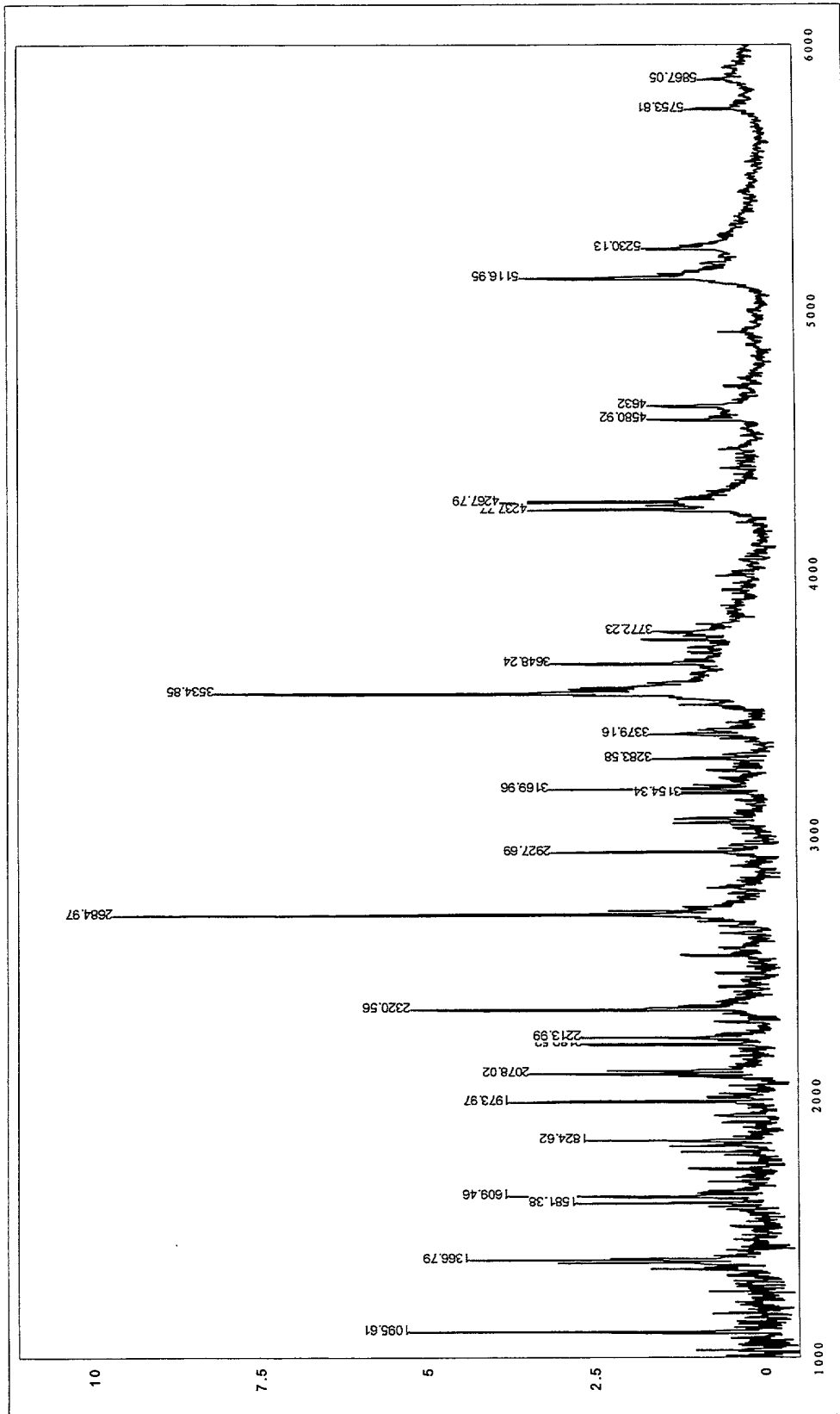


FIG. 5

10066359.013400

Sheet 6 of 27

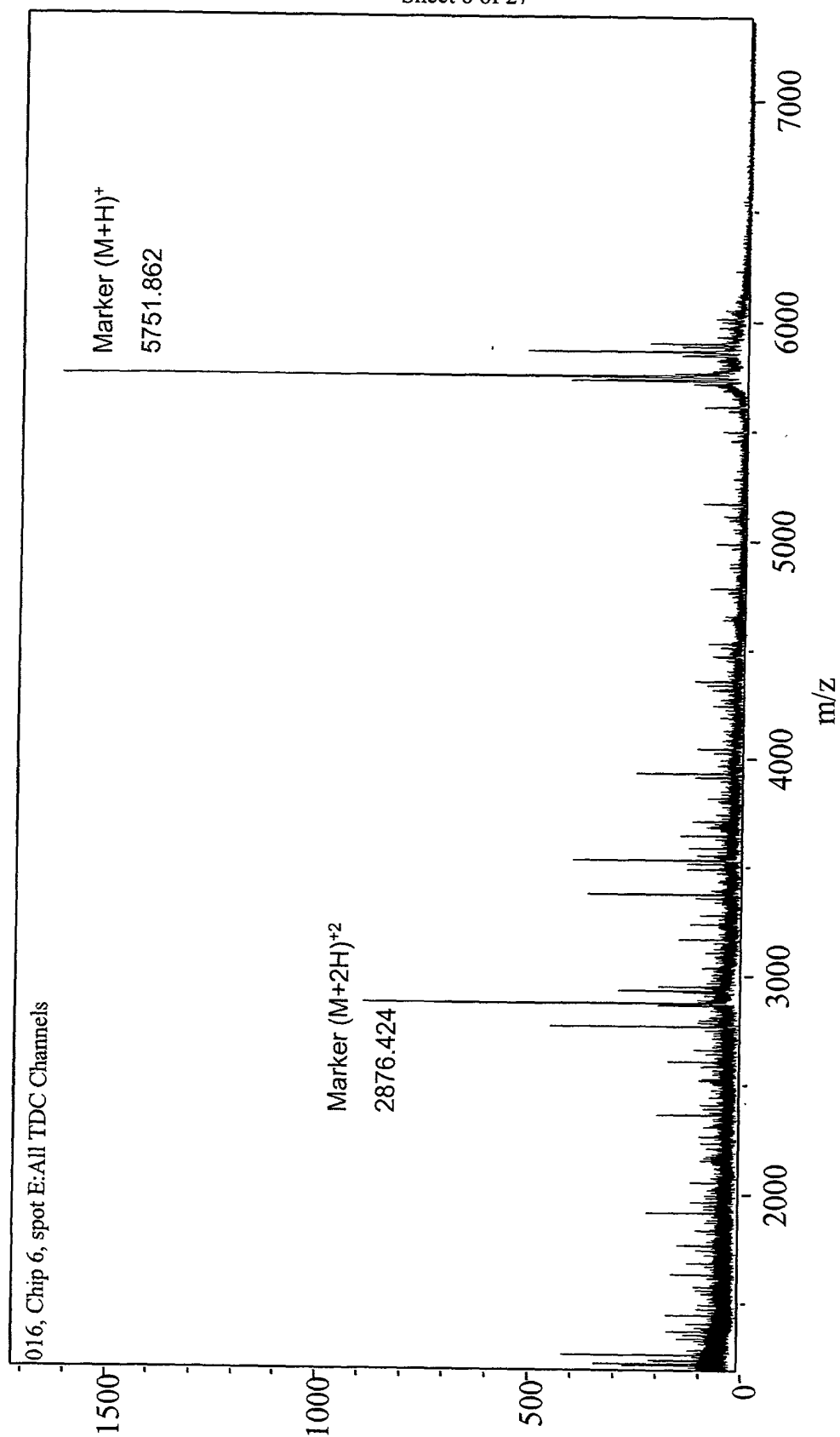


FIG. 6

201610066690001

Sheet 7 of 27

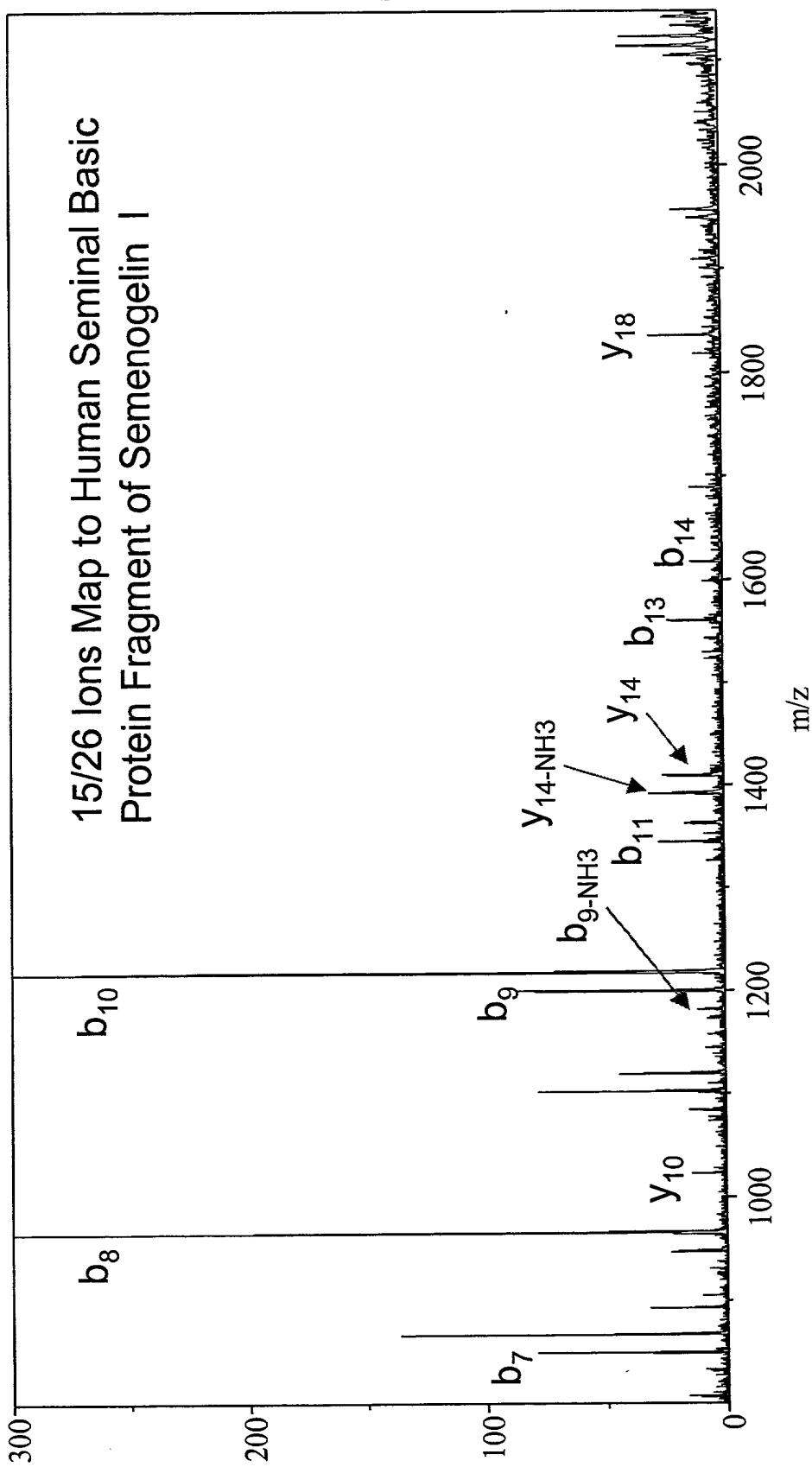


FIG. 7

Sheet 8 of 27

Retentate Mapping of a Peptide Map on a Reverse Phase ProteinChip® Array

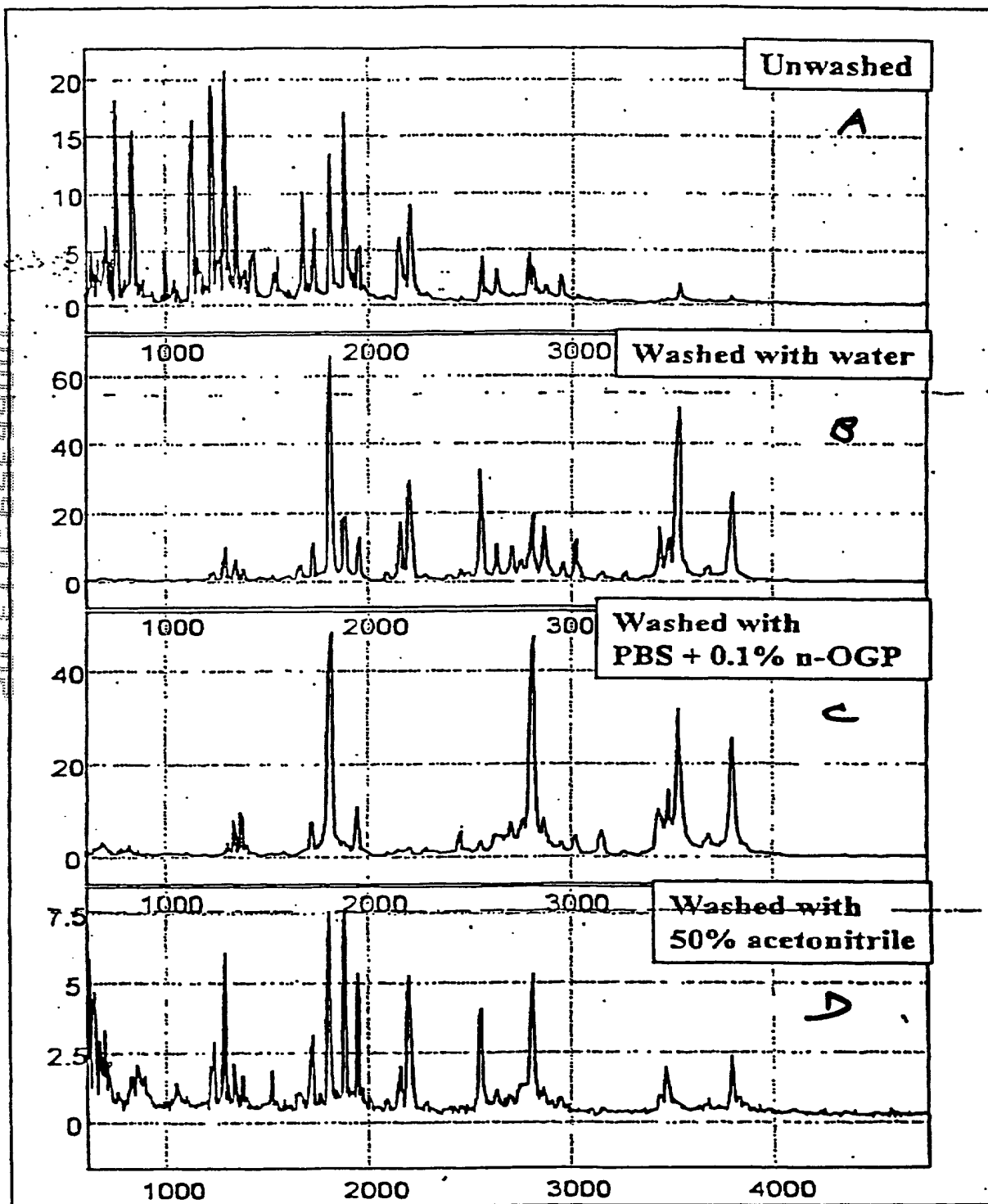


FIG. 8

Sheet 9 of 27

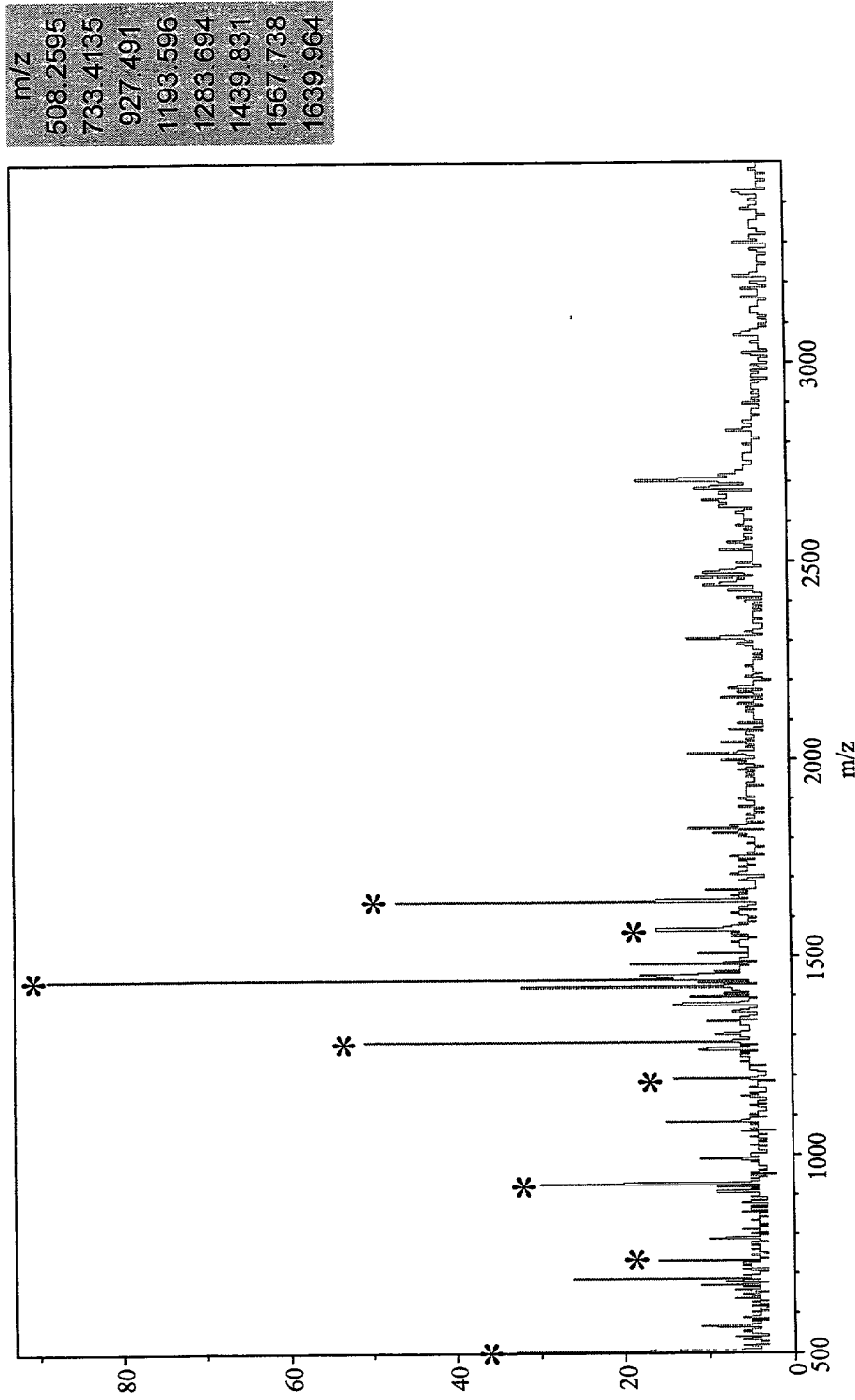


FIG. 9

m/z
508.2488
572.3584
689.3708
733.4133
906.4743
927.4924
1001.583
1083.596
1193.603
1283.707
1439.806
1595.88
1639.933
1810.986
1823.904
1897.078

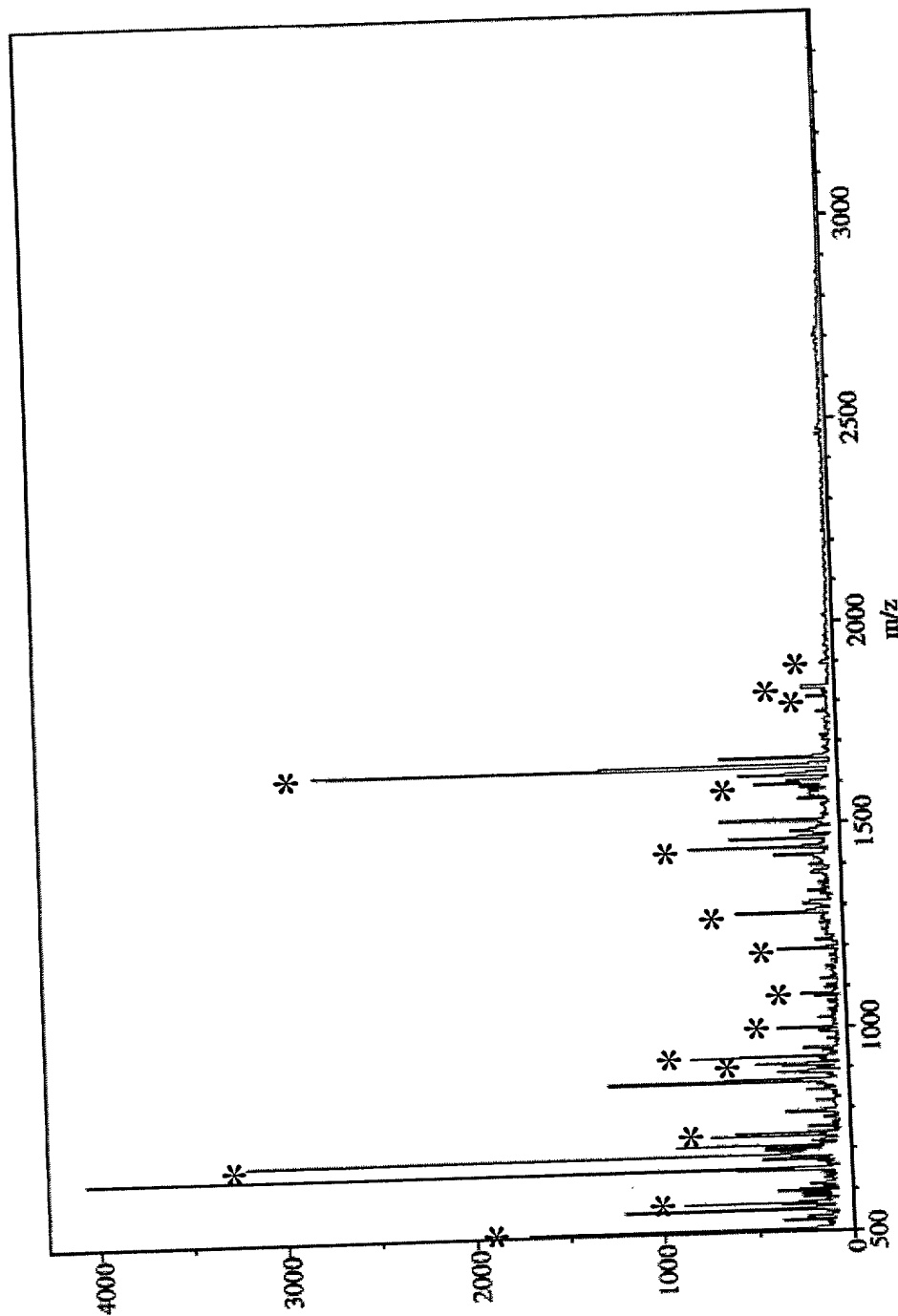


FIG. 10

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Sheet 11 of 27

Fragment	esidues	Cal. M/Z	pI	H2O	pH3	pH4	pH5	pH6	pH7	pH8	pH9	All Conditions
30	204-207	K/F...R/A	6	508.2524	508.2523	508.2507	508.2488	508.2471	508.2477	508.247	508.2471	508.2518
27-28	194-197	R/Q...R/C	12	572.3638	572.3628	572.3623	572.3584	572.3581	572.3586	572.3576	572.3581	572.3628
32	211-216	K/A...R/L	9.8	689.3766	689.376	689.3753	689.3708	689.37	689.3693	689.3692	689.37	689.3728
26	187-193	K/V...R/Q	9.7	733.4199	733.4219	733.421	733.4202	733.4193	733.4159	733.4093	733.4193	733.4208
66	457-463	R/L...K/T	6.7	847.5069	847.5069	847.5087		847.4989	847.5046		847.4989	841.4598
33-34	217-223	R/L...K/A	10	906.4828	906.4808	906.4814	906.4786	906.4743	906.4594			847.5038
24-25	180-186	K/L...K/V	6.1	927.4875	927.488	927.497	927.4961	927.4924	927.4889	927.4886	927.4905	906.4718
28-29	196-203	R/L...K/F	9.5	990.5469		990.5759						918.5188
19	137-143	K/Y...R/R	6	1001.61	1001.592	1001.592	1001.585	1001.583	1001.568	1001.581	1001.582	927.4938
25-26	185-193	R/E...R/Q	8.8									990.5578
31-32	208-216	R/A...R/L	11									1001.5888
26-27	187-195	K/V...R/L	12									
69	473-481	K/C...R/R	6	1083.597	1083.602	1083.602	1083.601	1083.596	1083.59	1083.605	1083.575	1083.5948
19-20	137-144	K/Y...R/H	8.6	1193.609	1193.609	1193.611	1193.595	1193.603	1193.596	1193.593	1193.6	1138.5678
29-30	198-207	R/C...R/A	8.2	1249.624	1249.624	1249.624	1249.624	1249.624	1249.624	1249.624	1249.624	1193.6018
36993	36901	-D...R/F	6.9	1283.726	1283.714	1283.714	1283.712	1283.707	1283.701	1283.697	1283.712	1249.6208
36954	37215	R/F...K/G	5.4	1305.707	1305.689	1305.689	1305.689	1305.689	1305.689	1305.689	1305.689	1283.7108
50	336-346	R/H...R/L	6.7	1439.812	1439.815	1439.819	1439.812	1439.806	1439.801	1439.794	1439.81	1305.7158
55	377-387	K/H...K/Z	5.3									1362.6718
8	65-76	K/S...K/V	5.3									1439.8118
49-50	335-346	R/R...R/L	8.7	1555.906	1555.908	1555.982	1555.991	1555.98				1587.7428
18-19	133-143	K/F...R/R	8.5	1639.943	1639.942	1639.944	1639.94	1639.933	1639.928	1639.928	1639.928	1595.9268
68-70	470-482	K/V...R/P	10.8	1692.942	1692.942							1777.1058
48	322-334	K/D...R/R	4.4	1750.952	1750.951	1750.951	1811.035	1810.986	1811.007	1810.992		1639.9378
50-51	336-349	R/H...K/E	8.6	1823.912	1823.912	1823.907	1823.9	1823.904				1692.9418
74-77	519-533	K/Q...K/P	10	1962.931	1962.931			1897.078				1750.9738
59-60	411-425	R/K...R/S	8.7	2301.035	2301.035							1811.0088
65	443-456	R/M...R/L	4.4			2441.13						1823.8998
35-36	224-238	K/A...K/V	4.7									1897.0748
33-35	217-231	R/L...K/L	8.5									1962.9478
66-68	457-472	R/L...K/C	8.2									2301.0818
70-71	482-497	R/R...K/A	6									2441.0998
60-61	412-429	K/V...K/V	8.7									2457.1828
14-16	115-131	K/L...K/K	4.4									2701.2448
47-48	316-334	K/N...R/R	4.7									3211.5538
36995	36911	-D...K/G	6.3									
37-39	239-260	K/V...K/Y	4.9									
47-49	316-335	K/N...R/H	6.1									
14-18	115-136	K/L...K/Y	6.2									
63-65	434-456	R/C...R/L	4.9									
36-39	232-260	K/L...K/Y	4.9									
51-54	347-376	R/L...K/H	4.7									
Total Peptides				14	24	23	16	16	14	12	12	34
Sequence Coverage (%)				18	34	29	21	20	17	15	9	45

FIG. 11

Sheet 12 of 27

fragment residues	Cal. M/Z	pI	H2O	pH3	pH4	pH5	pH6	pH7	pH8	pH9	All Conditions
30	204-207	K/F...R/A	508.2518	6							508.25183
27-28	194-197	R/Q...R/C	572.3628	12							572.36283
32	211-216	K/A...R/L	689.3728	9.8							689.37283
26	187-193	K/V...R/Q	733.4208	9.7							733.42083
66	457-463	R/L...K/T	841.4598	6.7							
33-34	217-223	R/L...K/A	847.5038	10							
24-25	180-186	K/L...K/V	906.4718	6.1							
28-29	196-203	R/L...K/F	918.5188	9.5							
19	137-143	K/Y...R/R	927.4938	6							
25-26	185-193	R/E...R/Q	990.5578	8.8							
31-32	208-216	R/A...R/L	1001.589	11							
26-27	187-195	K/V...R/L	1017.58	12							
69	473-481	K/C...R/R	1024.455	6							
19-20	137-144	K/Y...R/H	1083.595	8.6							
29-30	198-207	R/C...R/A	1138.568	8.2							
36893	36901	-D...R/F	1193.602	6.9							
36954	37215	R/F...K/G	1249.621	5.4							
50	336-346	R/H...R/L	1283.711	6.7							
55	377-387	K/H...K/Z	1305.716	5.3							
8	65-76	K/S...K/V	1362.672	5.3							
49-50	335-346	R/R...R/L	1439.812	8.7							
18-19	133-143	K/F...R/R	1445.758	8.5							
68-70	470-482	K/V...R/P	1508.767	10.8							
48	322-334	K/D...R/R	1587.743	4.4							
50-51	336-349	R/H...K/E	1595.927	8.6							
74-77	519-533	K/Q...K/P	1777.106	10							
59-60	411-425	R/K...R/S	1639.938	8.7							
65	443-456	R/M...R/L	1667.813	4.4							
35-36	224-238	K/A...K/V	1692.942	4.7							
33-35	217-231	R/L...K/L	1750.974	8.5							
66-68	457-472	R/L...K/C	1811.009	8.2							
70-71	482-497	R/R...K/A	1823.9	6							
60-61	412-429	K/V...K/V	1897.075	8.7							
14-16	115-131	K/L...K/K	1962.948	4.4							
47-48	316-334	K/N...R/R	2301.082	4.7							
36895	36911	-D...K/G	2424.205	6.3							
37-39	239-260	K/V...K/Y	2441.1	4.9							
47-49	316-335	K/N...R/H	2457.183	6.1							
14-18	115-136	K/L...K/Y	2608.306	6.2							
63-65	434-456	R/C...R/L	2701.245	4.9							
36-39	232-260	K/L...K/Y	3211.554	4.9							
51-54	347-376	R/L...K/H	3420.579	4.7							

Total Peptides
Sequence Coverage (%)

FIG. 12

Sheet 13 of 27

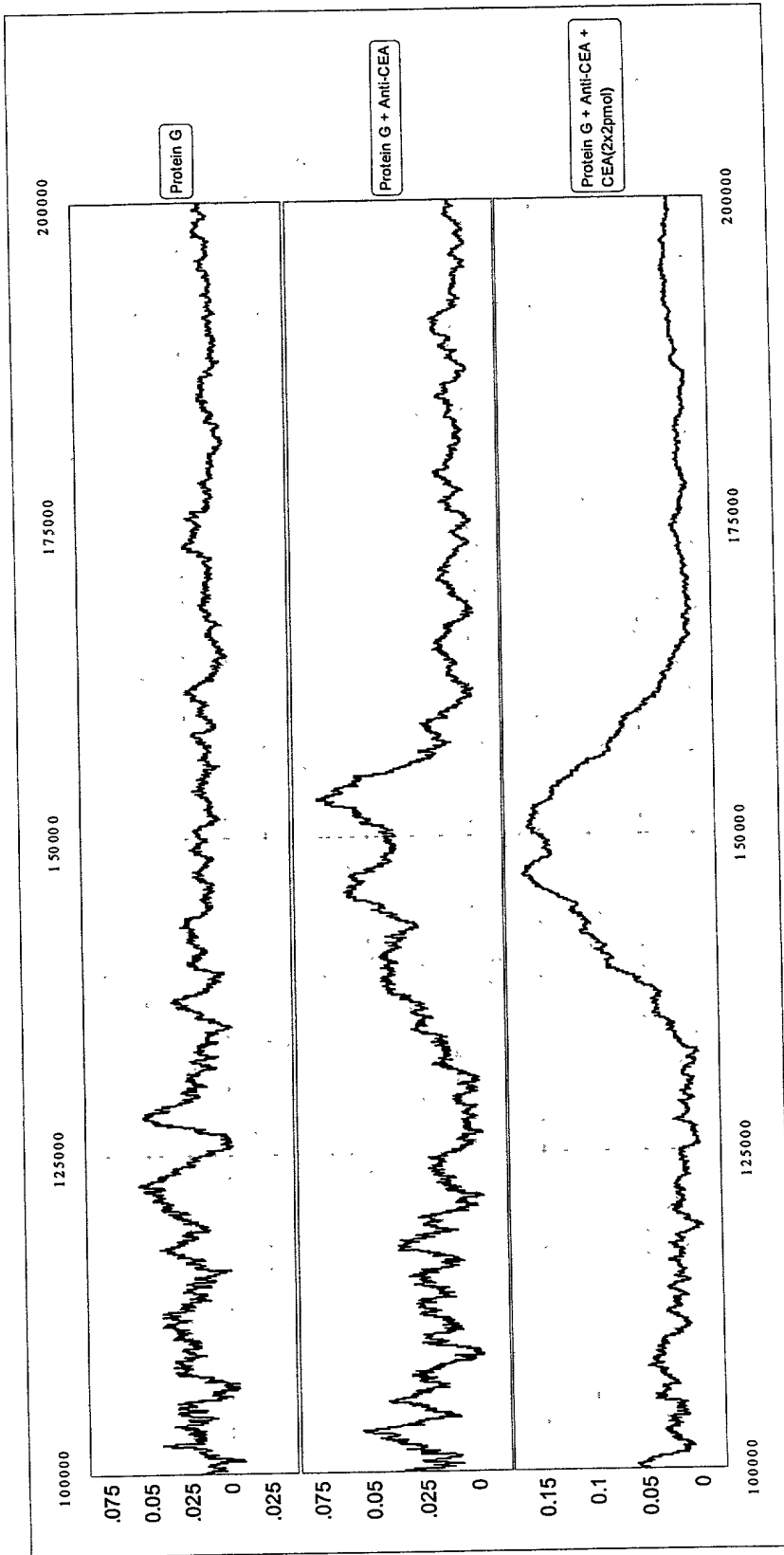


FIG. 13

Sheet 14 of 27

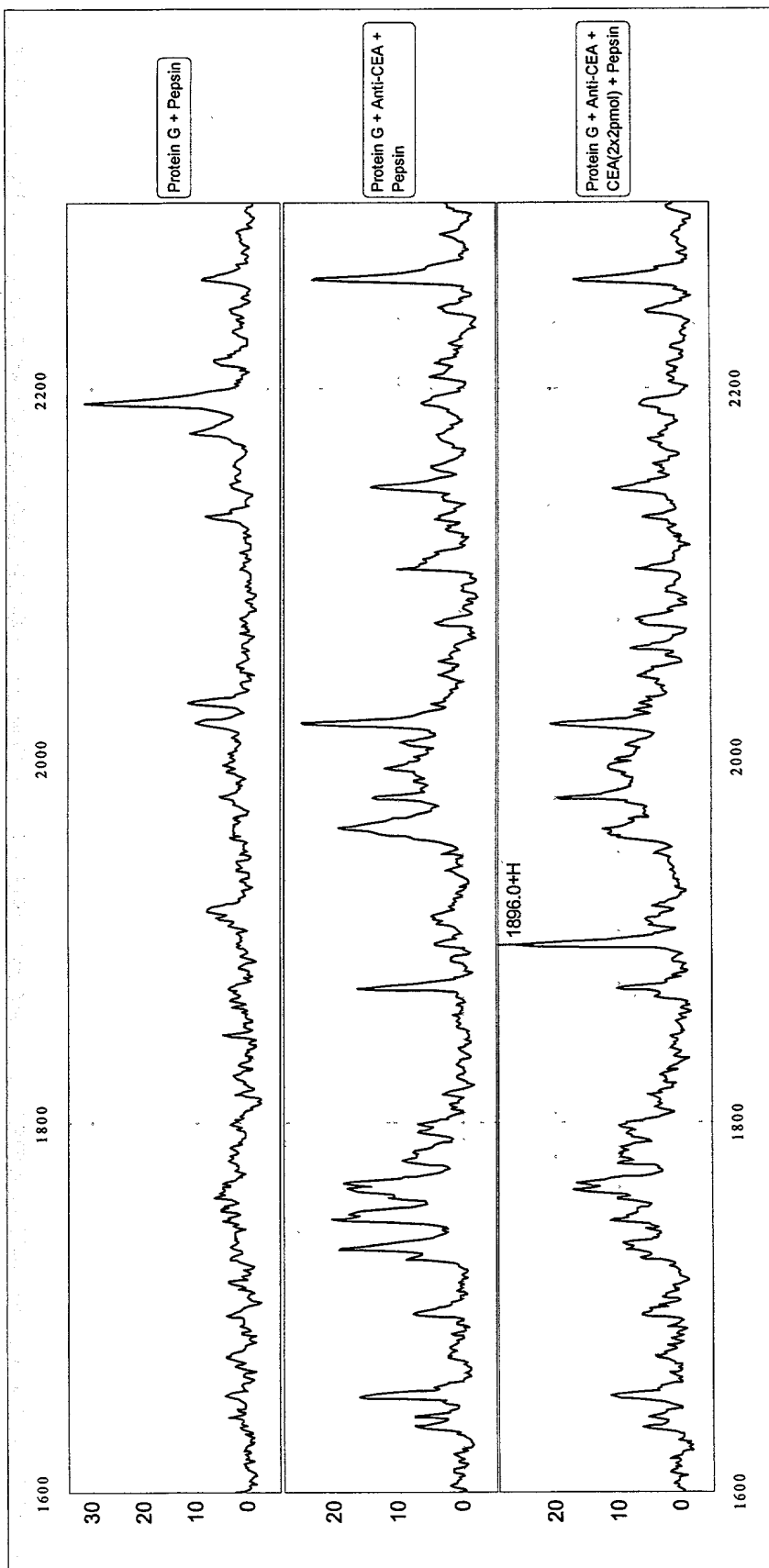


FIG. 14

Sheet 15 of 27

YVIGTQQATAYSGREPGP

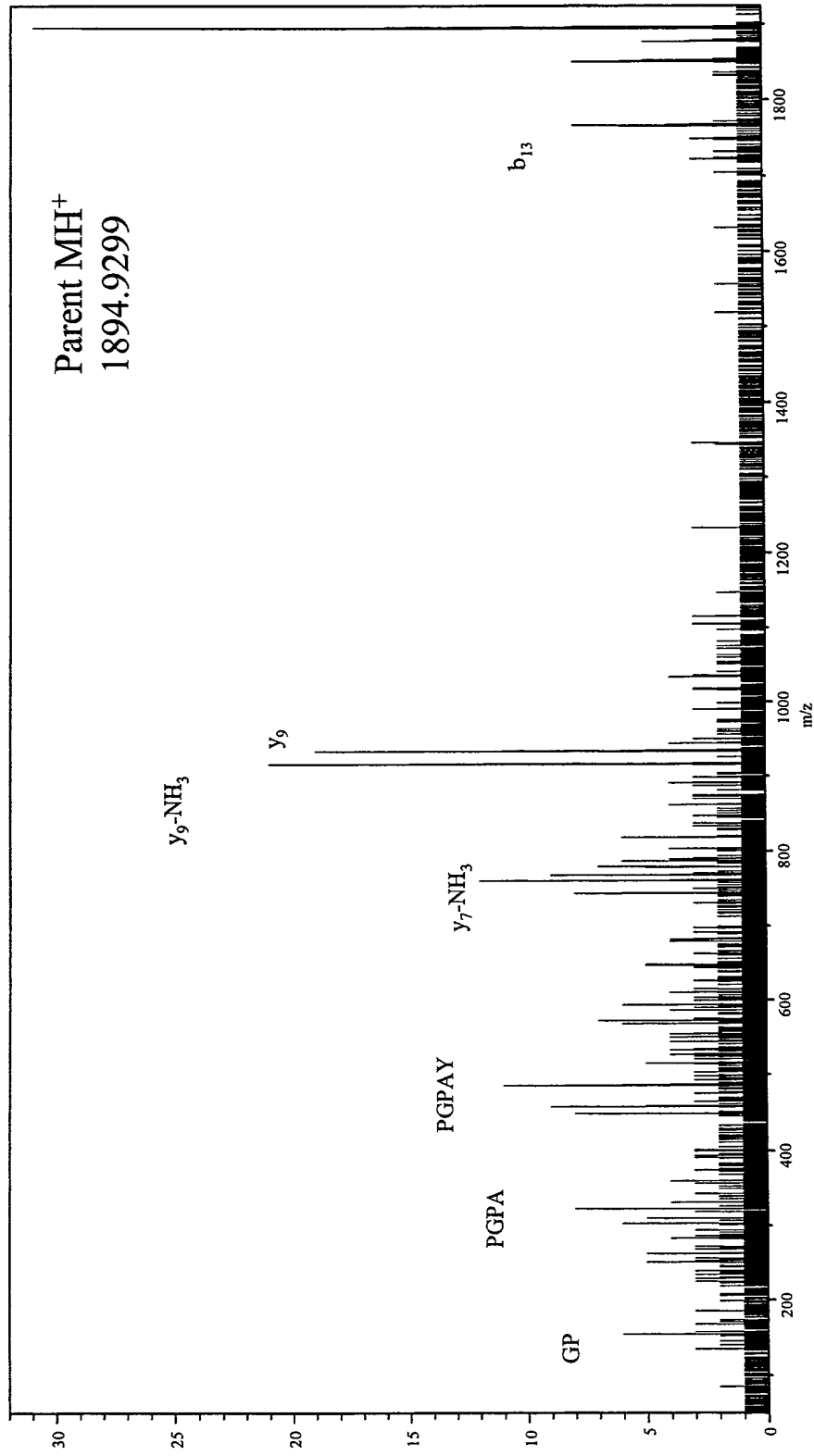


FIG. 15

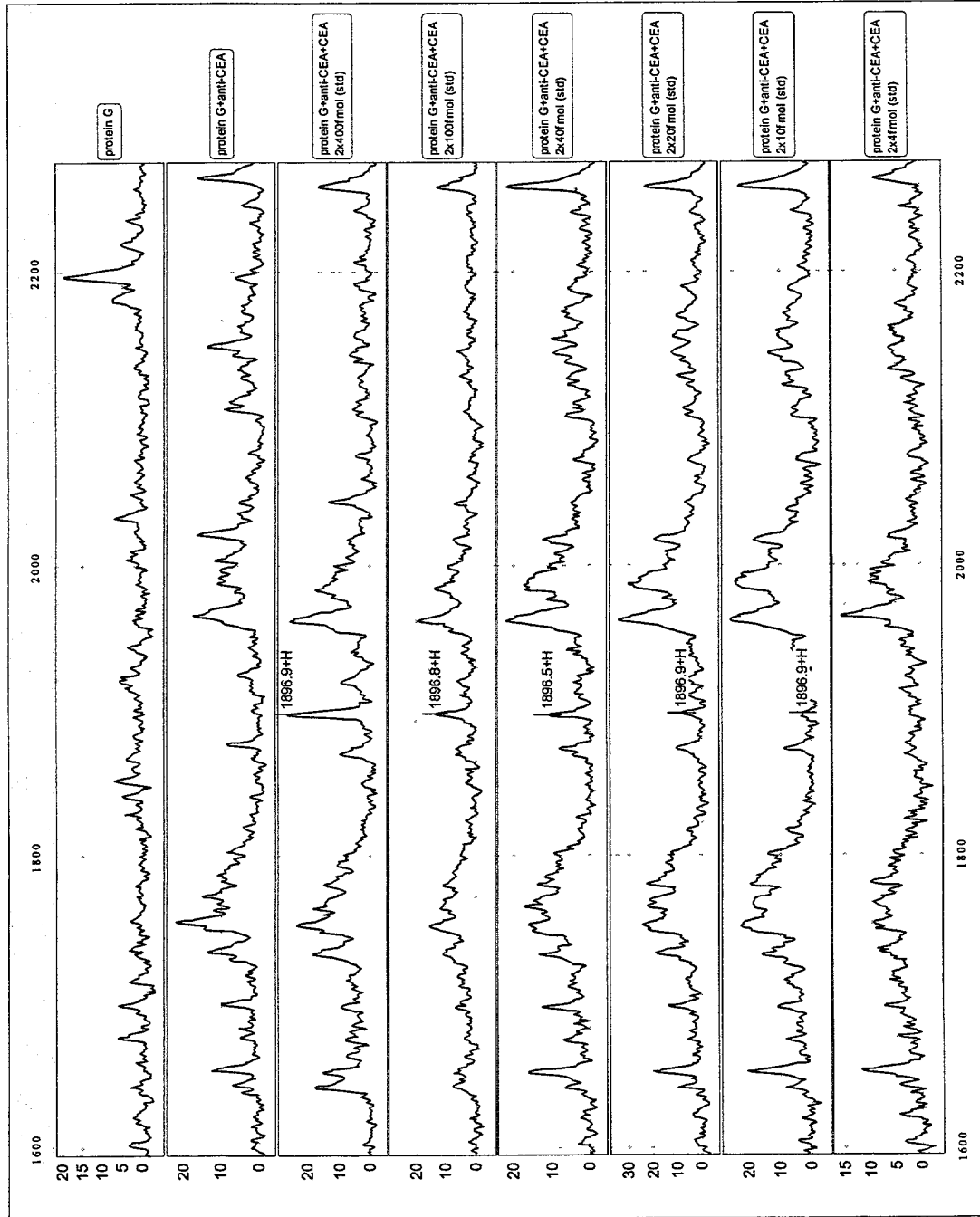


FIG. 16

Quantitative Antigen Capture

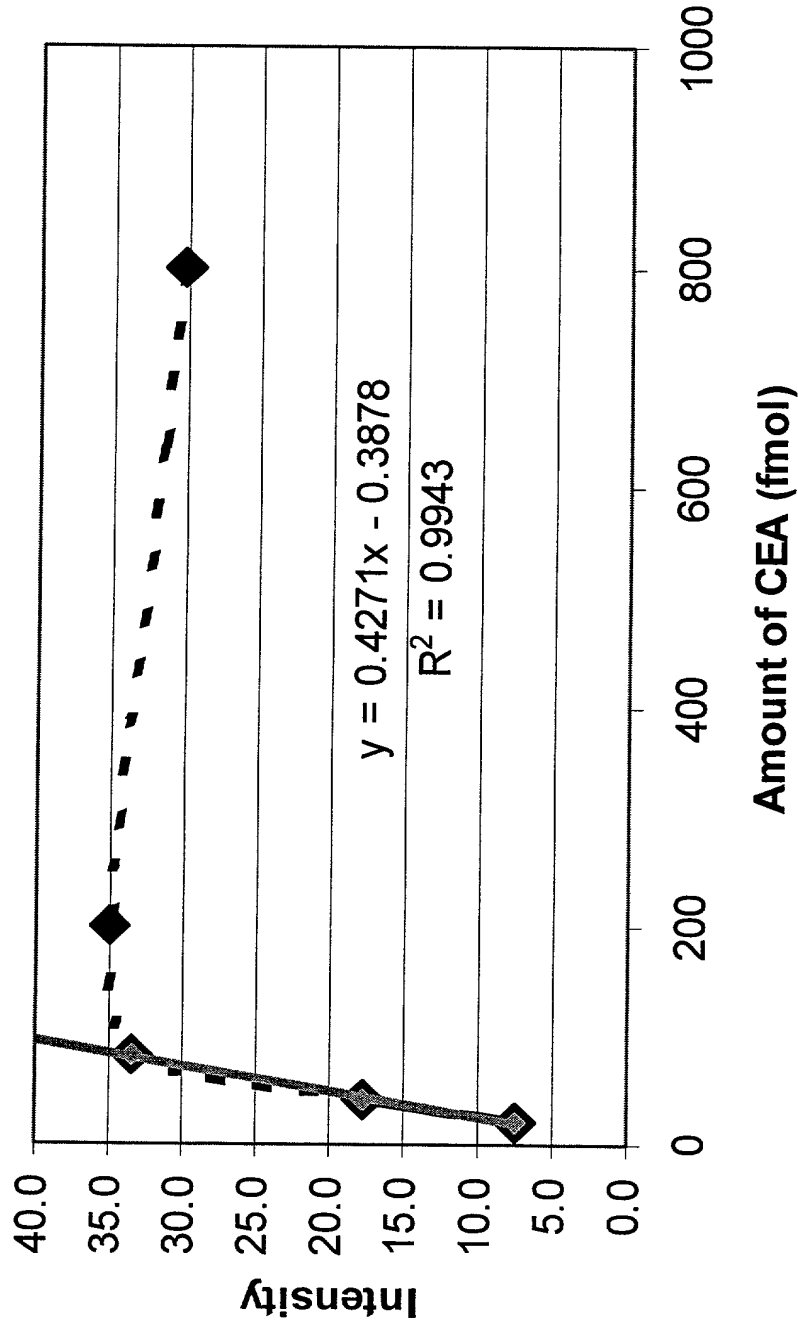


FIG. 17

Sheet 18 of 27

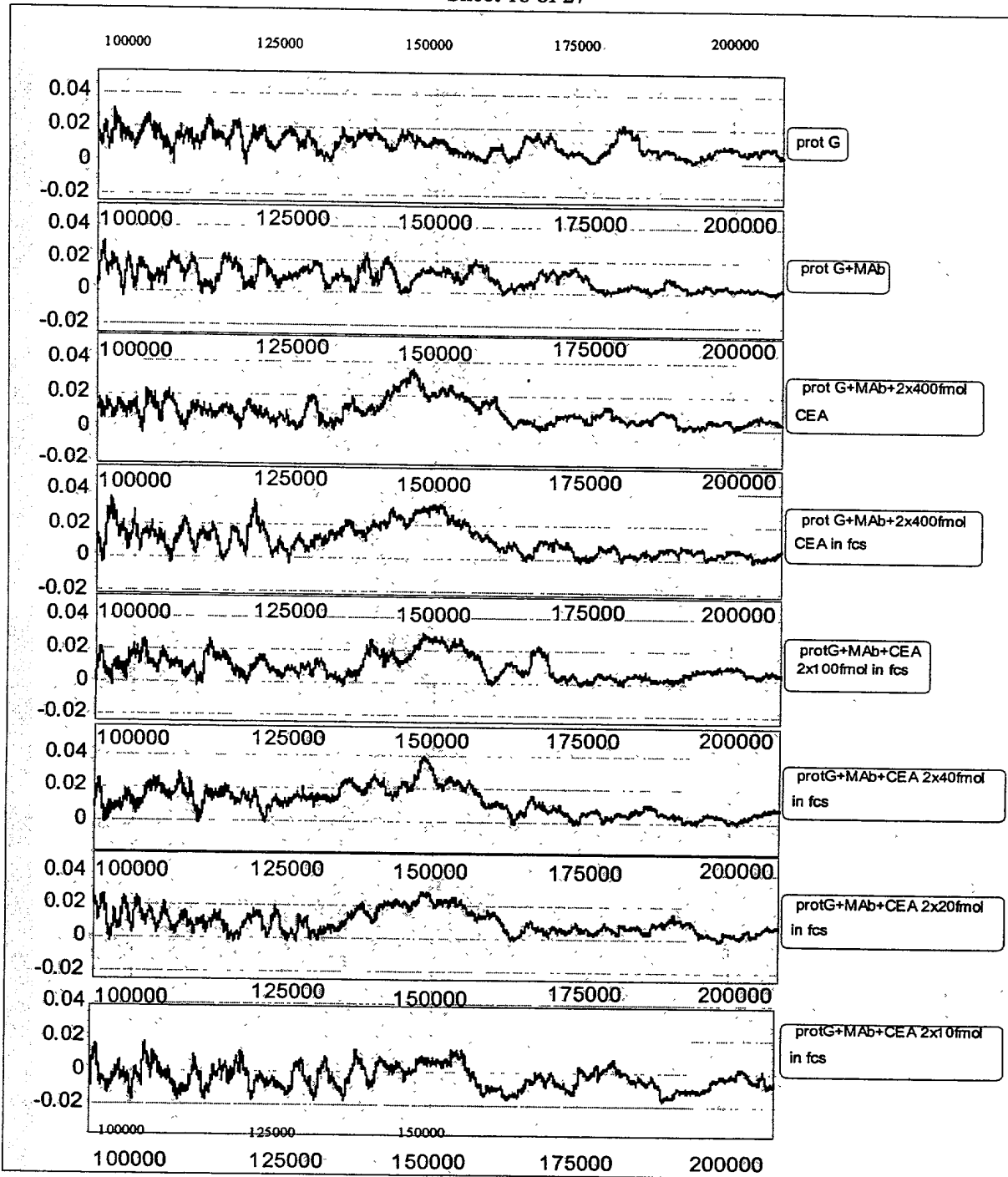


FIG. 18

Sheet 19 of 27

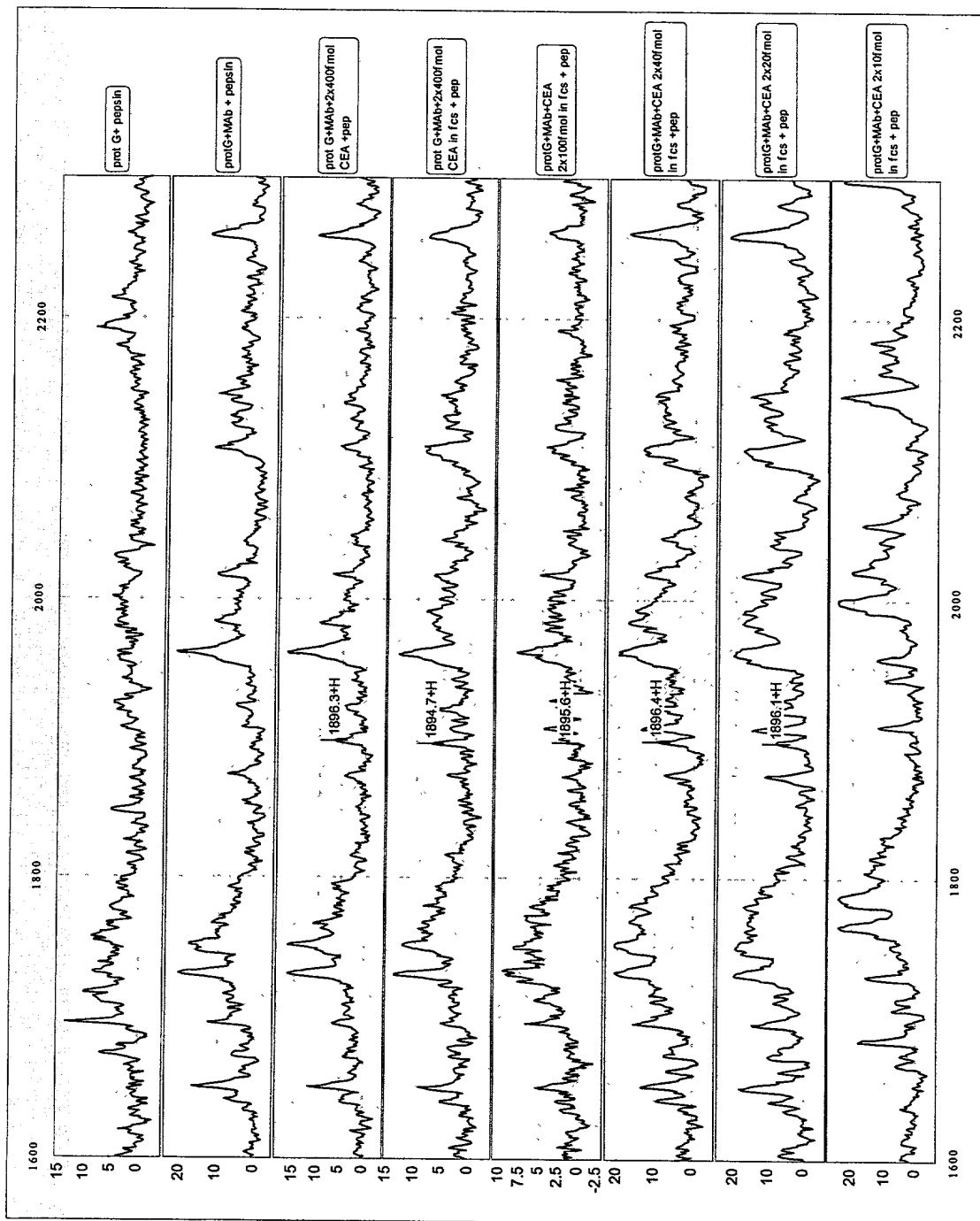


FIG. 19

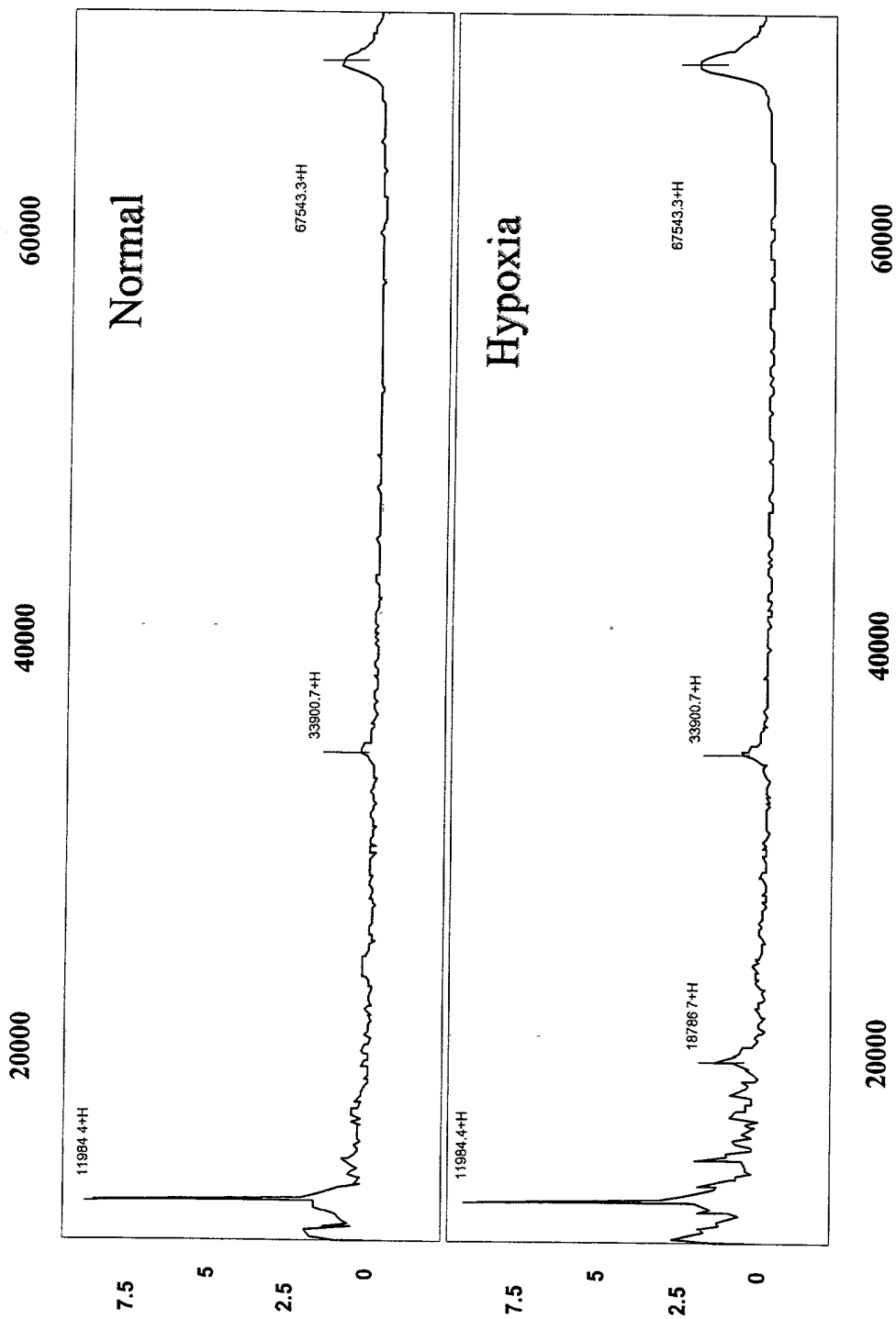
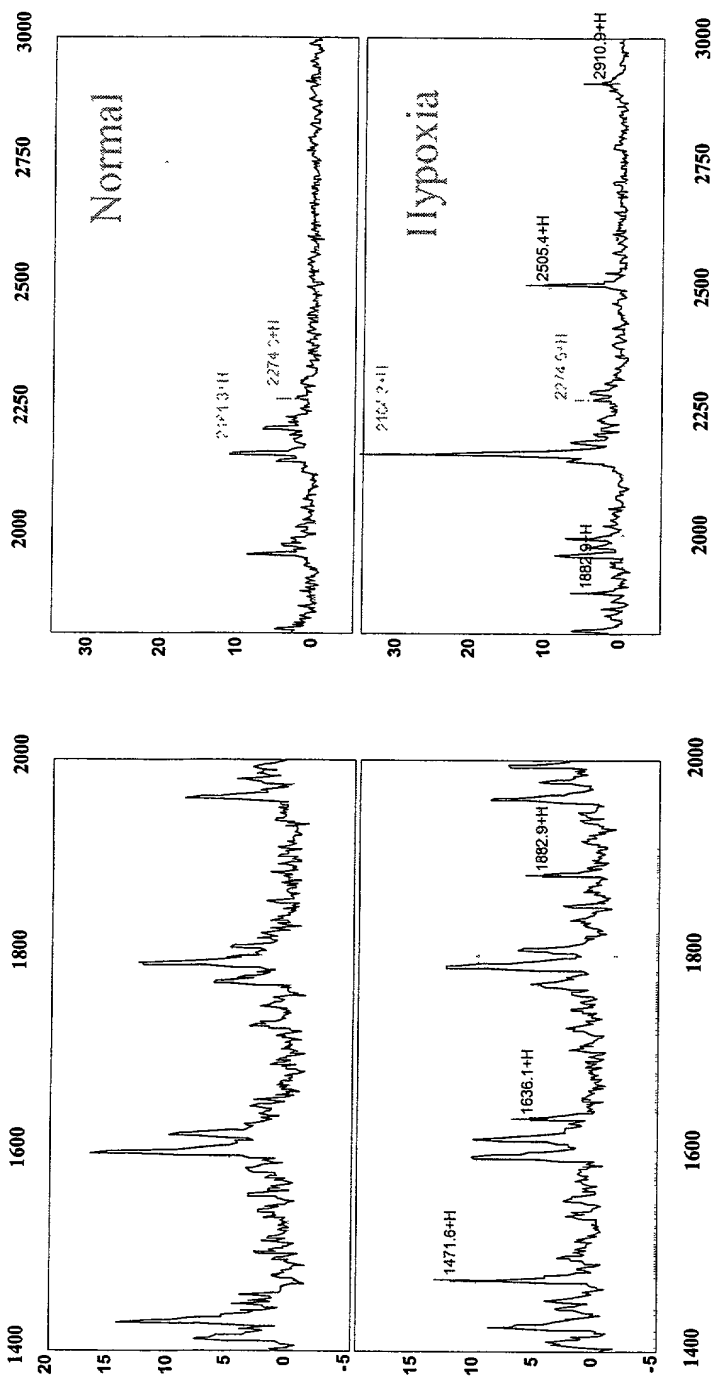


FIG. 20



Fragments generated from trypsin autolysis: 2164.3, 2274.6

FIG. 21

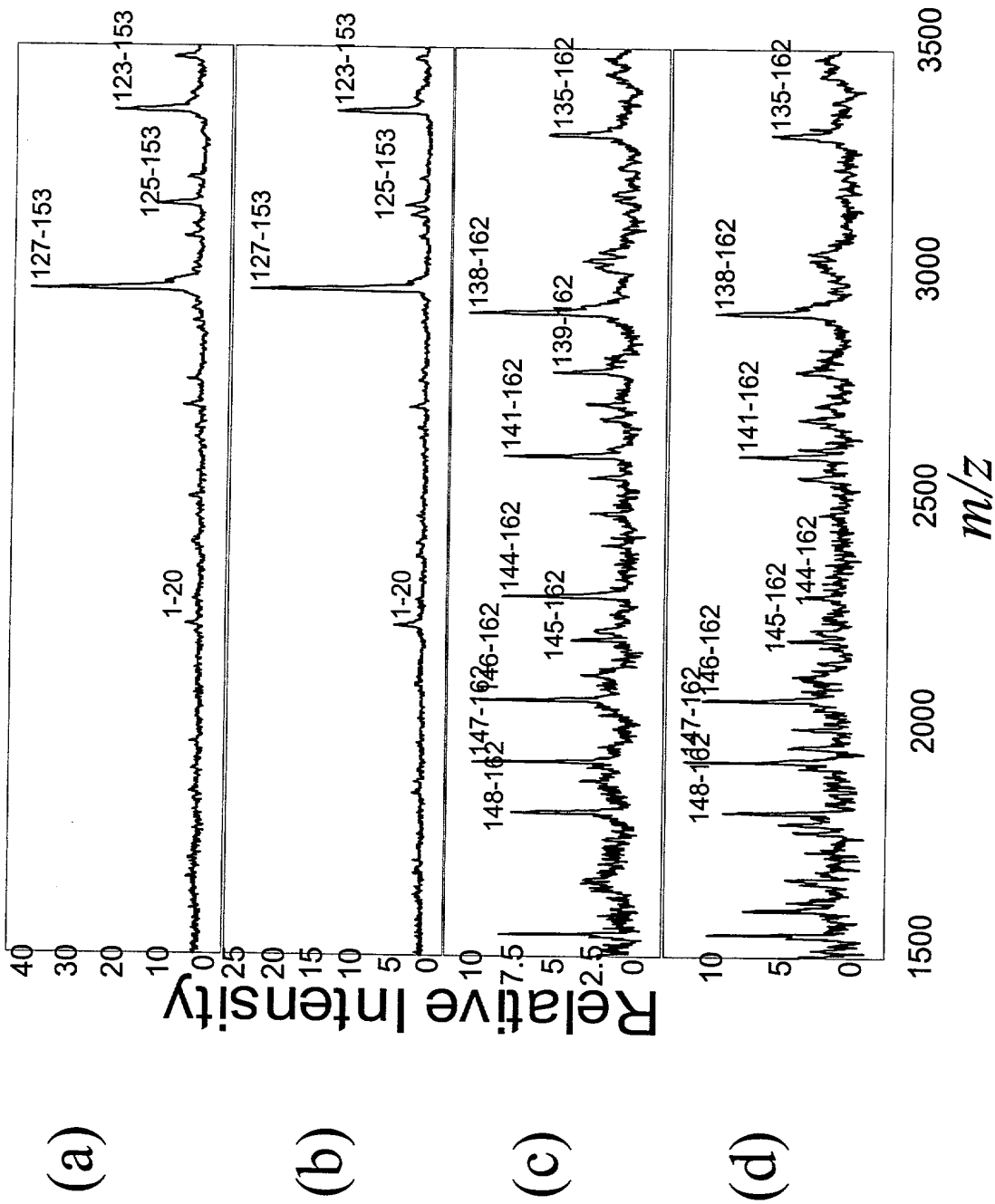
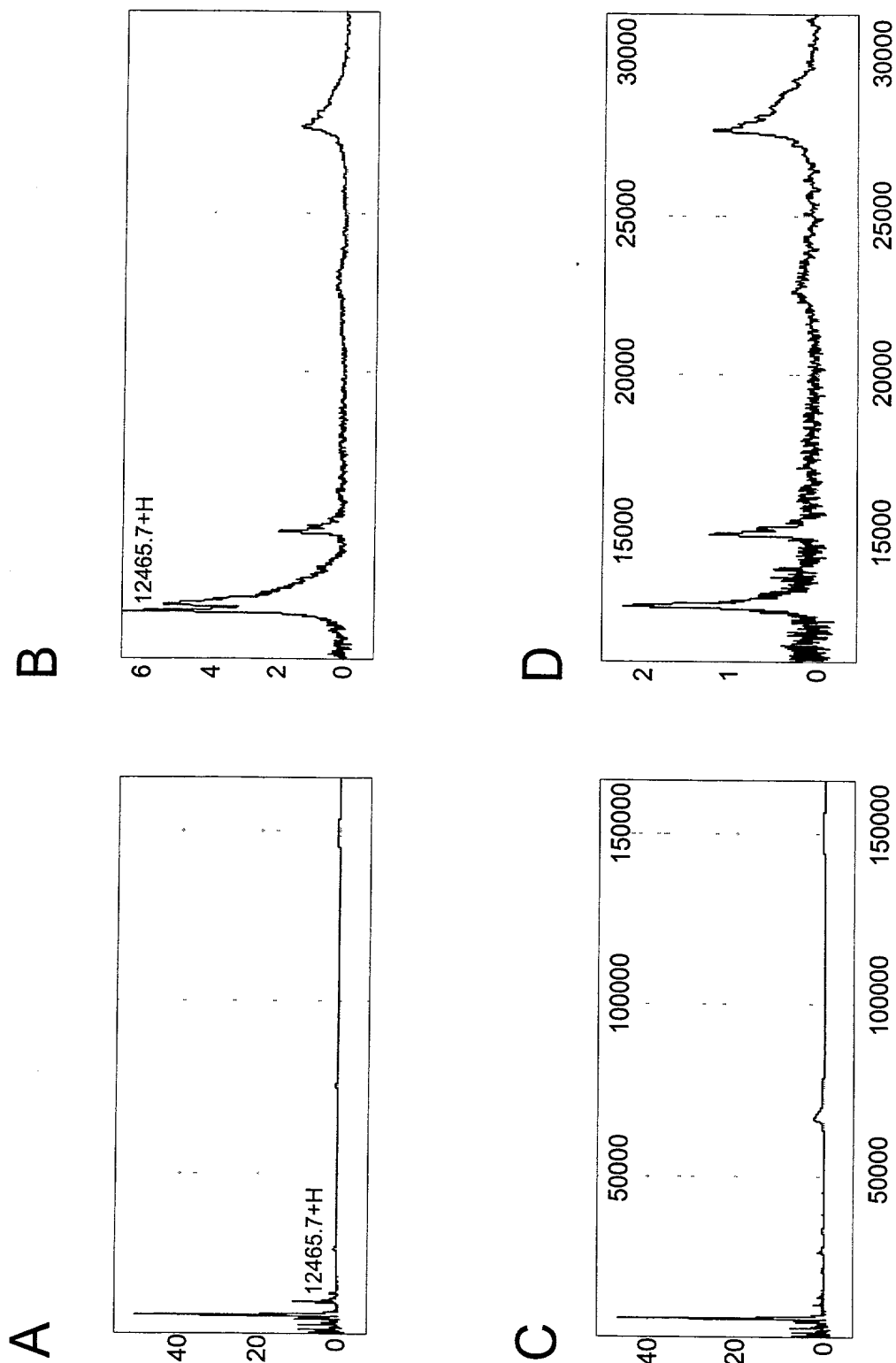


FIG. 22



Sheet 24 of 27

Single MS

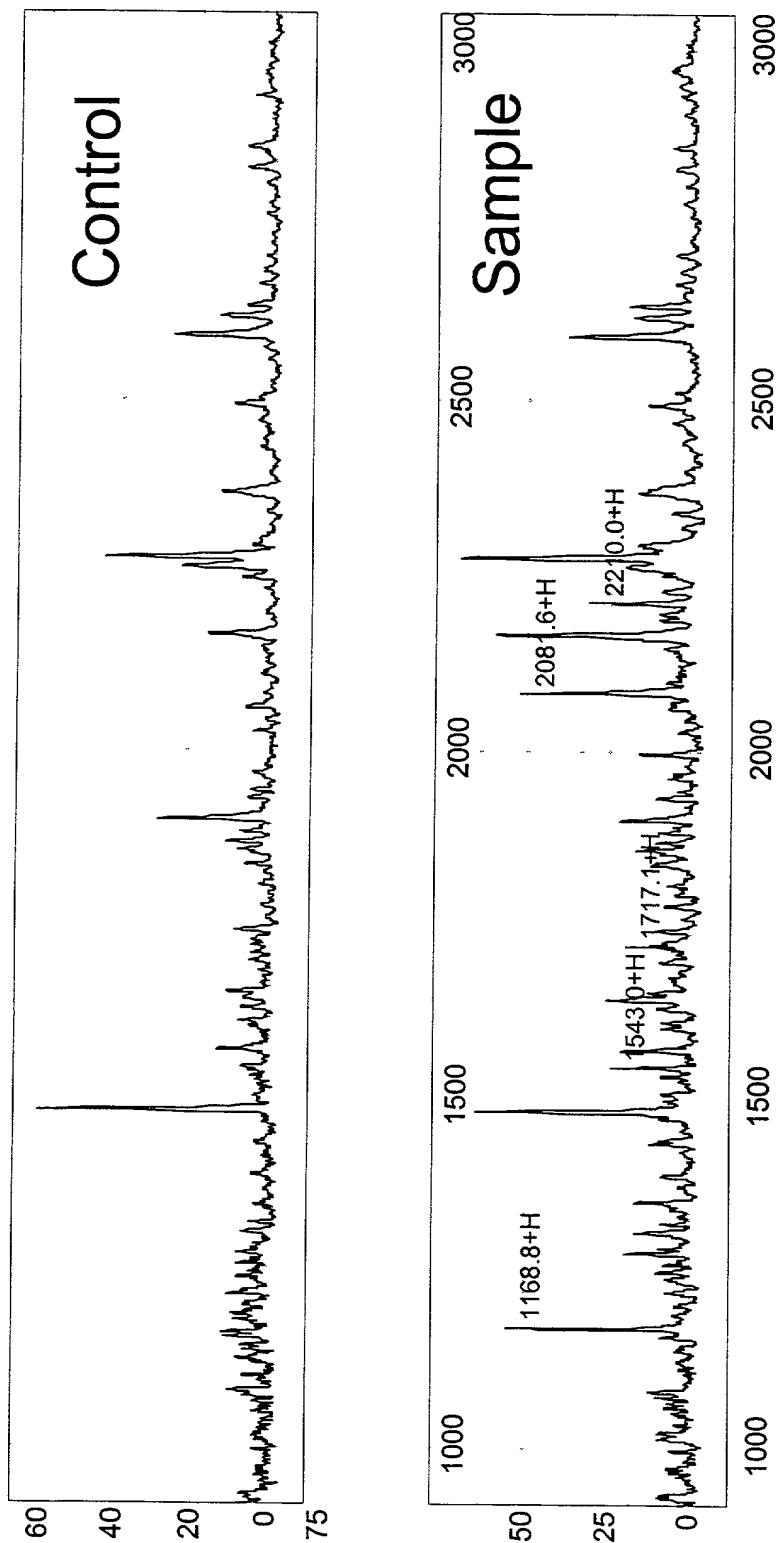


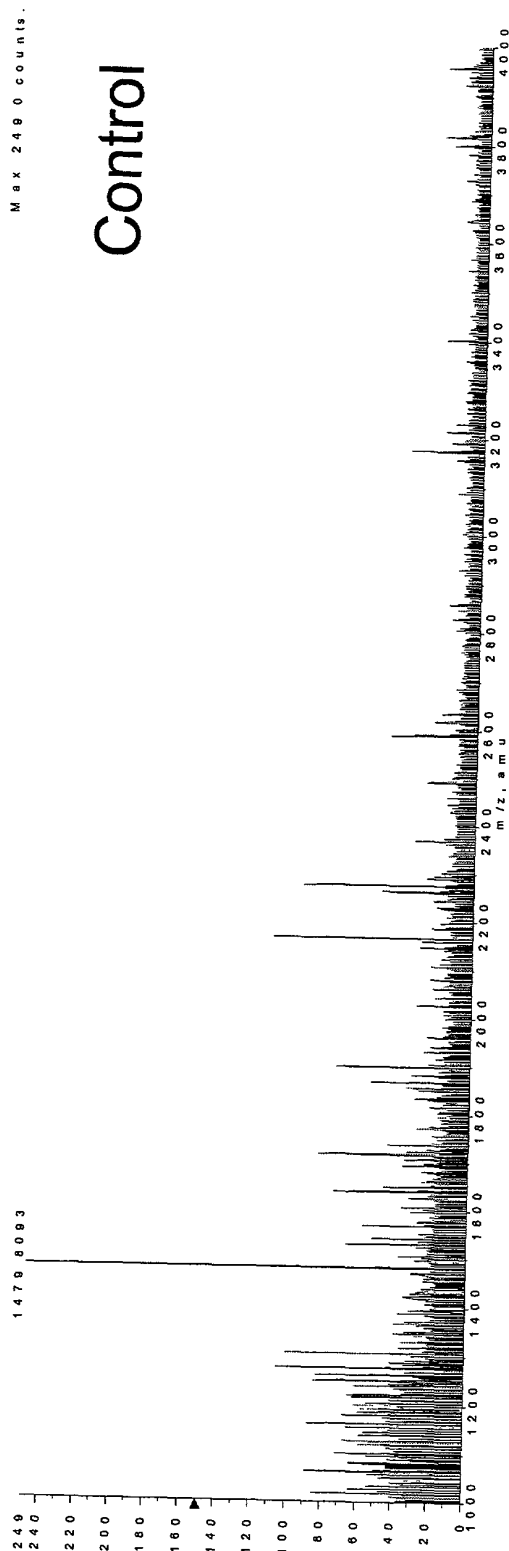
FIG. 24

Sheet 25 of 27

QqTOF Tandem MS

A

TOF MS 60 MCA scans from FCS Trypsin Digest w/IF



B

TOF MS 60 MCA scans from FCS-CytoC 6 5pmol Trypsin Digest w/IF

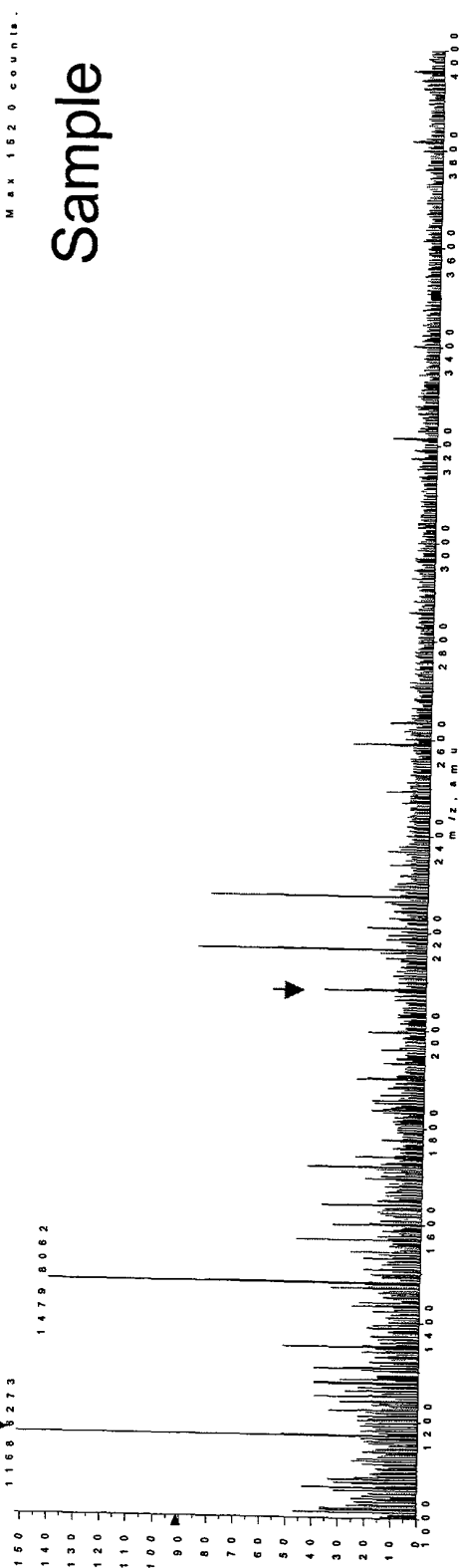


FIG. 25

Sheet 26 of 27

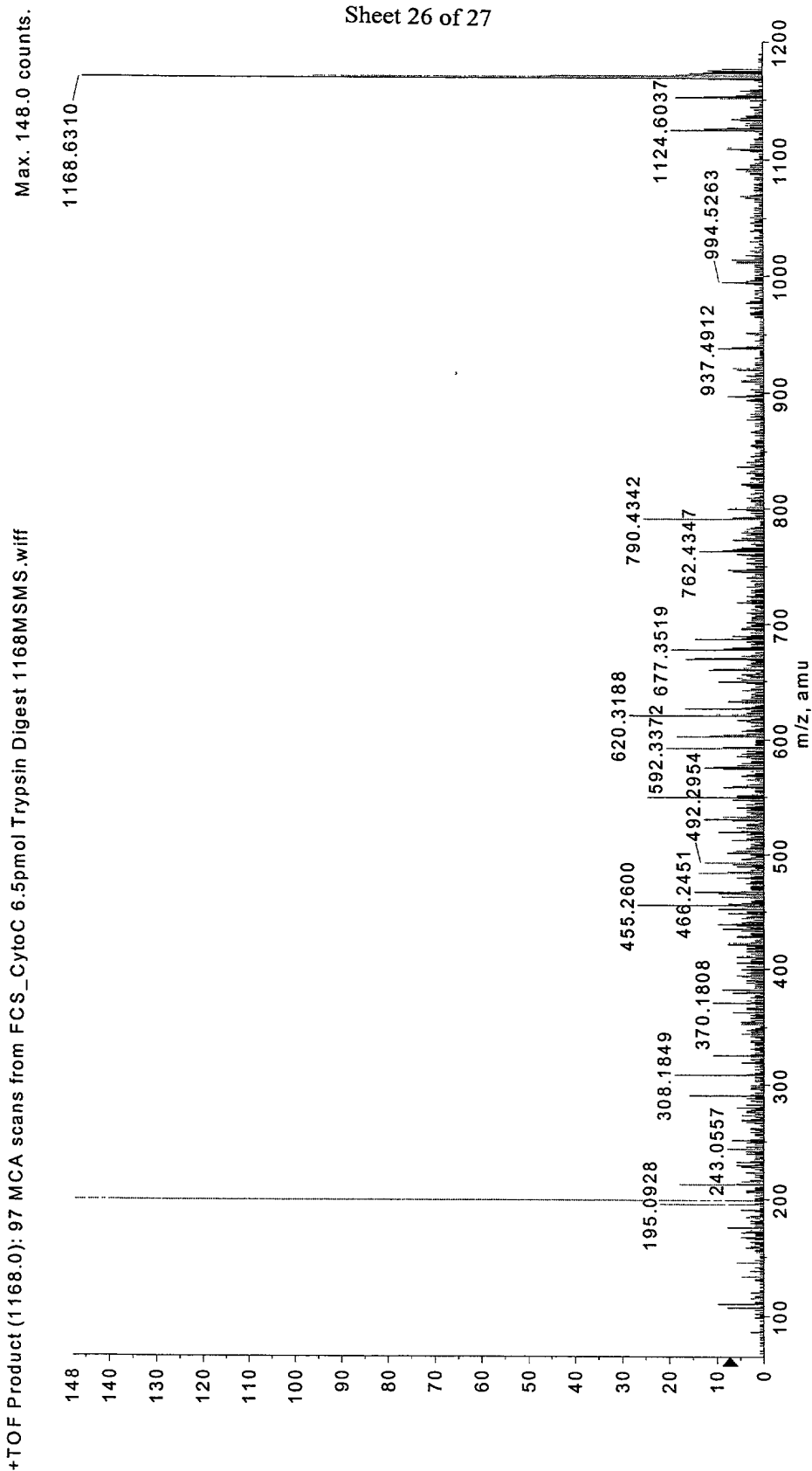


FIG. 26

1168 MS/MS

2015-09-09 15:55:00

Sheet 27 of 27

2011-10-20 16:55:00

MS-Tag Search Results

Press stop on your browser if you wish to abort this MS-Tag search prematurely
Sample ID (comment): Apo A-1 1040 AKPVLEDLR
Database searched: NCBIhm.12.5.2001
Full Molecular Weight range: 810480 entries
Full pI range: 810480 entries

Pre searches select 810480 entries

Ion Types Considered: a-NH3, b, b-H2O, b-H2O+y-NH3, y, y-H2O, i, im

Search Peptide Masses Digest Max # Missed Cysteines Peptide
Mode are Used Cleavages Modified by N-terminus C-terminus
identity monoisotopic Trypsin 3 unmodified Hydrogen (H) Free Acid (OH)

Number of sequences passing through parent mass filter: 18092

MS-Tag search selects 33 entries (results displayed for top 25 matches)

Parent mass: 1168.6310 (± 50.0000 ppm)

14 Fragment Ions used in search: 175.10, 195.09, 243.06, 308.18, 455.26, 549.51, 620.32, 669.35, 677.35, 762.43, 790.43, 937.49, 994.53, 1108.60 (± 50.00 ppm)

Max # Unmatched Ions = 7

Result Summary

Rank	Unmatched Ions	Sequence	MTF Calculated Error (Da)	MTF Protein Error (ppm)	Species	NCBIhm.12.5.2001 Accession #	Protein Name
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11808.9 / 9.63	HOMO SAPIENS	15929398	(BC015130) cytochrome c
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11888.0 / 9.52	UNREADABLE	14782885	>gi14782885 ref XP_043240.1 (XM_043240) hypothetical protein XP_043240 Homo sapiens
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11757.8 / 9.59	UNREADABLE	4139715	>gi4139715 pdb 1G1W Solution Structure Of Reduced Horse Heart Cytochrome C, Nmr, Minimized Average Structure
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11703.6 / 9.47	CHICKENS, HEART, PEPTIDE, 104 AA	914118	apocytochrome c
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11825.8 / 9.54	HORSES, HEART, PEPTIDE, 104 AA	914117	apocytochrome c
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11814.8 / 9.59	UNREADABLE	4139756	>gi4139756 pdb 1WEJ Chain F, IgG1 Fab Fragment (Of B8 Antibody) Complexed With Horse Cytochrome C At 1.8 A Resolution
1	3/14	(K)IGPNLHGLFGR(K)	1168.6227	7.1 11474.3 / 9.61	GUINEA PIG, CERNATIVE SEQUENCE	483111	cytochrome c

FIG. 27